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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
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08/653,294 05/24/96 CLAYBERGER C 286002020023

HM22/1101

EXAMINER

KATE H MURASHIGE
MORRISON & FOERSTER
2000 PENNSYLVANIA AVENUE NW
WASHINGTON DC 20006-1888

DIBRINO, M

ART UNIT	PAPER NUMBER
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1644

(47)

DATE MAILED:

11/01/01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks



UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER NUMBER

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). A computer readable form (CRF) of the sequence listing was submitted. However, the CRF could not be processed by the Scientific and Technical Information Center (STIC) for the reason(s) set forth on the attached CRF Diskette Problem Report.

Applicant is given ONE MONTH, or THIRTY DAYS, whichever is longer, from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached CRF Diskette Problem Report with the reply.

Any inquiry concerning this communication should be directed to Examiner Ron Schwadron, Ph.D., Art Unit 1644, whose telephone number is (703) 308-4680. Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.

RONALD B. SCHWADRON
PRIMARY EXAMINER
GROUP 1800

Ron Schwadron, Ph.D.
Art Unit 1644

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):



1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.



2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).



3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).



4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."



5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).



6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).



7. Other: _____

Applicant Must Provide:



An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".



An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.



A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

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Raw Sequence Listing Error Summary

TECH CENTER 1600/2900

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>08/653,294B</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleic <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input checked="" type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/653,294B

DATE: 06/20/2001
TIME: 11:11:44
TECH CENTER 1600/2900

Input Set : D:\28600-20200.txt
Output Set: N:\CRF3\06202001\H653294B.raw

3 <110> APPLICANT: Stanford University
4 Clayberger, Carol
5 Krensky, Alan
6 Buelow, Roland
8 <120> TITLE OF INVENTION: IMMUNOMODULATING DIMERS
11 <130> FILE REFERENCE: 28600-20200.23
13 <140> CURRENT APPLICATION NUMBER: 08/653,294B
14 <141> CURRENT FILING DATE: 1996-05-24
16 <150> PRIOR APPLICATION NUMBER: US 08/222,851
17 <151> PRIOR FILING DATE: 1994-04-05
19 <150> PRIOR APPLICATION NUMBER: US 07/844,716
20 <151> PRIOR FILING DATE: 1992-03-02
22 <150> PRIOR APPLICATION NUMBER: US 07/755,584
23 <151> PRIOR FILING DATE: 1991-09-03
25 <150> PRIOR APPLICATION NUMBER: US 07/672,147
26 <151> PRIOR FILING DATE: 1991-03-19
28 <150> PRIOR APPLICATION NUMBER: US 07/561,246
29 <151> PRIOR FILING DATE: 1990-07-30
31 <150> PRIOR APPLICATION NUMBER: US 07/008,846
32 <151> PRIOR FILING DATE: 1987-01-30
34 <160> NUMBER OF SEQ ID NOS: 42
36 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply
Corrected Diskette Needed

pp 1-3

Please
consult

Sequence Rules,
for valid
format

ERRORED SEQUENCES

38 <210> SEQ ID NO: 1
39 <211> LENGTH: 10
40 <212> TYPE: PRT
41 <213> ORGANISM: Human
43 <220> FEATURE:
44 <221> NAME/KEY: VARIANT
45 <222> LOCATION: (1)...(10)
46 <223> OTHER INFORMATION: Xaa⁽⁷⁾ = E or V;
47 Xaa⁽⁷⁾ = D, S or N;
48 Xaa⁽⁷⁾ = R or G;
49 Xaa⁽⁷⁾ = I or N;
W--> 50 Xaa⁽⁷⁾ is a hydrophobic or small amino acid;
W--> 51 Xaa⁽⁷⁾ = R or L;
W--> 52 Xaa⁽⁷⁾ = G or R;
W--> 53 Xaa⁽⁷⁾ = is a hydrophobic or small amino acid.
55 <400> SEQUENCE: 1
56 Arg Xaa⁽⁶⁾ Xaa⁽⁷⁾ Leu Xaa⁽⁸⁾ Xaa⁽⁹⁾ Xaa⁽¹⁰⁾ Xaa⁽¹¹⁾ Xaa⁽¹²⁾
E--> 57 1 5 10
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 10
61 <212> TYPE: PRT

Reword the statement:

Xaa at location 2

Per 1.823 of Sequence Rules,
the maximum number of
lines in <223> response
is 4; insert a <220> after the
4th line and insert <223> at
beginning of 5th line

invalid - do not
insert number next to
Xaa's; just show
Xaa

Misaligned amino
acid nos - see
item 3 on Error
summary sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/653,294B

DATE: 06/20/2001
TIME: 11:11:44

Input Set : D:\28600-20200.txt
Output Set: N:\CRF3\06202001\H653294B.raw

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TECH CENTER 1600/2900

62 <213> ORGANISM: Human
 64 <220> FEATURE:
 65 <221> NAME/KEY: VARIANT
 66 <222> LOCATION: (1)...(10)
 67 <223> OTHER INFORMATION: Xaa⁷⁶ = E or V;
 68 Xaa⁷⁷ = D, S or N;
 69 Xaa⁷⁹ = R or G;
 70 Xaa⁸⁰ = I or N;
 W--> 71 Xaa⁸¹ is a hydrophobic or small amino acid;
 W--> 72 Xaa⁸² = R or L;
 W--> 73 Xaa⁸³ = G or R;
 W--> 74 Xaa⁸⁴ = is a hydrophobic or small amino acid.
 76 <400> SEQUENCE: 2
 E--> 77 Xaa⁸⁴ Xaa⁸³ Xaa⁸² Xaa⁸¹ Xaa⁷⁹ Leu Xaa⁷⁷ Xaa⁷⁶ Arg
 E--> 78 1 5 10 misaligned nos.
 80 <210> SEQ ID NO: 3
 81 <211> LENGTH: 10 9 shown
 82 <212> TYPE: PRT
 83 <213> ORGANISM: Human
 85 <220> FEATURE:
 86 <221> NAME/KEY: VARIANT
 87 <222> LOCATION: (1)...(10)
 88 <223> OTHER INFORMATION: Xaa¹ = Any Amino Acid;
 89 Xaa² = N or I; or any amino acid of at least five carbon atoms;
 90 Xaa³ = I or hydrophobic or small amino acid;
 91 Xaa⁴ = R or any aliphatic amino acid of at least five carbon atoms;
 W--> 92 Xaa⁵ = G or R or any aliphatic amino acid;
 W--> 93 Xaa⁶ = any amino acid, hydrophobic or small.
 95 <400> SEQUENCE: 3
 96 Arg Glu Xaa¹ Leu Arg Xaa² Xaa³ Xaa⁴ Xaa⁵
 E--> 97 1 5 10
 433 <210> SEQ ID NO: 38
 434 <211> LENGTH: 10
 435 <212> TYPE: PRT
 436 <213> ORGANISM: Human
 438 <220> FEATURE:
 439 <221> NAME/KEY: VARIANT
 440 <222> LOCATION: (1)...(10)
 441 <223> OTHER INFORMATION: Xaa⁷⁷ = D, S or N;
 442 Xaa⁸⁰ = I or N;
 443 Xaa⁸¹ = A or L;
 444 Xaa⁸² = R or L;
 W--> 445 Xaa⁸³ = G or R.
 447 <400> SEQUENCE: 38
 E--> 448 Arg Glu Xaa⁷⁷ Leu Arg Xaa⁸⁰ Xaa⁸¹ Xaa⁸² Xaa⁸³ Tyr
 E--> 449 1 5 10 misaligned nos.
 451 <210> SEQ ID NO: 39
 452 <211> LENGTH: 10
 453 <212> TYPE: PRT

same error

same error

same error

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/653,294B

DATE: 06/20/2001
TIME: 11:11:44

Input Set : D:\28600-20200.txt
Output Set: N:\CRF3\06202001\H653294B.raw

454 <213> ORGANISM: Human
 456 <220> FEATURE:
 457 <221> NAME/KEY: VARIANT
 458 <222> LOCATION: (1)...(10)
 459 <223> OTHER INFORMATION: Xaa⁷⁷ = D, S or N;
 460 Xaa⁸⁰ = I or N;
 461 Xaa⁸¹ = A or L;
 462 Xaa⁸² = R or L;
 W--> 463 Xaa⁸³ = G or R.
 E--> 465 <400> SEQUENCE: 39
 E--> 466 Tyr Xaa⁸³ Xaa⁸² Xaa⁸¹ Xaa⁸⁰ Arg Leu Xaa⁷⁷
 E--> 467 1 5 10

VERIFICATION SUMMARY

PATENT APPLICATION: US/08/653,294B

DATE: 06/20/2001

TIME: 11:11:45

Input Set : D:\28600-20200.txt

Output Set: N:\CRF3\06202001\H653294B.raw

L:50 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:51 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:52 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:53 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:57 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:57 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:1
L:71 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:72 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:73 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:74 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:77 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:77 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:78 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:92 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:93 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:97 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:97 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:3
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:445 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:448 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:448 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:449 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
L:463 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:466 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:466 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:467 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39